

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:48:45 ; Search time 7.04242 Seconds

(without alignments)
1133.013 Million cell updates/sec

Title: US-09-988-971-2_COPY_94_176

Perfect score: 446

Sequence: 1 WLVEGLSRKNAEELLPCN.....WLTVSPRLTFPSLOALVDHY 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	254	57.0	505	1	TVHDC
2	242	54.3	512	1	TVHDC
3	241	54.0	503	1	TVHDC
4	241	54.0	512	1	TVHDC
5	241	54.0	512	1	TVHDC
6	240	53.8	281	2	TVHDC
7	240	53.8	503	1	TVHDC
8	232.5	52.1	505	2	TVHDC
9	228	51.1	509	1	TVHDC
10	227	50.9	509	1	TVHDC
11	224.5	50.3	499	1	TVHDC
12	223	50.0	507	1	TVHDC
13	217	48.7	544	2	TVHDC
14	215	48.2	537	1	TVHDC
15	214	48.0	528	1	TVHDC
16	214	48.0	541	1	TVHDC
17	212	47.5	529	1	TVHDC
18	212	47.5	543	1	TVHDC
19	211	47.3	541	2	TVHDC
20	209	46.9	534	1	TVHDC
21	208	46.6	517	2	TVHDC
22	207	46.4	539	2	TVHDC
23	207	46.4	663	1	TVHDC
24	206	46.2	534	1	TVHDC
25	206	46.0	517	1	TVHDC
26	205	45.7	517	1	TVHDC
27	203	45.5	537	1	TVHDC
28	199	44.6	392	2	TVHDC
29	197	44.2	537	2	TVHDC

ALIGNMENTS

30	197	44.2	542	2	A49114	protein-tyrosine k
31	195	43.7	536	2	S33569	protein-tyrosine k
32	186	41.7	526	1	TVFV60	protein-tyrosine k
33	186	41.7	533	1	TVCHS	protein-tyrosine k
34	186	41.7	557	1	TVFVS2	protein-tyrosine k
35	186	41.7	587	1	TVFVPS	protein-tyrosine k
36	185	41.5	568	1	TVFVSI	protein-tyrosine k
37	184.5	41.4	506	1	S24553	protein-tyrosine k
38	181	40.6	526	2	S26420	protein-tyrosine k
39	179	40.1	523	1	TVFVMT	protein-tyrosine k
40	179	40.1	545	2	S52313	protein-tyrosine k
41	179	40.1	546	2	S52314	protein-tyrosine k
42	177	39.7	526	1	TVFVPR	protein-tyrosine k
43	177	39.7	526	2	S15582	protein-tyrosine k
44	177	39.7	541	1	A43610	protein-tyrosine k
45	177	39.7	542	1	TVHDC	protein-tyrosine k

RESULT 1

TVHDC

C.Species: Homo sapiens (man)

C.Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999

C.Accession: A27811; A27812; J01149; C38268; S31103

R.Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Di

Mol. Cell. Biol. 7, 2267-2275, 1987

A>Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and

A.Reference number: A27811; PMID:8757942; PMID:3496523

A.Accession: A27811

A.Molecule type: mRNA

A.Residues: 1-505 <Q1>

A.Cross-references: GB:M16591

A.Note: the codon given for 3-Cys (TGC) is inconsistent with the authors' translation

Rizigler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.

Mol. Cell. Biol. 7, 2276-2285, 1987

A>Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h

A.Reference number: A27812; PMID:8757943; PMID:3453117

A.Accession: A27812

A.Molecule type: mRNA

A.Residues: 1-505 <Q1>

A.Cross-references: GB:M16592; NID:9183913; PIDN:AAA52644.1; PID:9306833

A.Hirderzky, D.; Streibhardt, K.; Ruebsamen-Waigmann, H.

Gene 113, 275-280, 1992

A>Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase

A.Reference number: J01149; PMID:92241680; PMID:1572549

A.Accession: J01149

A.Molecule type: DNA

A.Residues: 157-505 <HRA>

A.Cross-references: EMBL:X59741

R.Partanen, J.; Maelkela, T.P.; Allitalo, R.; Lehtvaestaho, H.; Allitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A.Reference number: A38268; PMID:91062389; PMID:2247464

A.Accession: C38268

A.Molecule type: mRNA

A.Residues: 362-417 <PAR>

C.Genes:

A.Gene: GDB:HCK

A.Cross-references: GDB:119303; OMIM:142370

A.Map position: 20q11-20q12

A.Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1

C.Function:

A.Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho

F:2-505/Product: protein-tyrosine kinase hck #status predicted <Mat>

F:64-112/Domain: SH3 homology <SH3>

F:123-220/Domain: SH2 homology <SH2>

F:239-497/Domain: protein kinase homology <KIN>

RESULT 4
I56160

I56160
protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat

C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 28-Jan-2000
 C/Accession: A27282; A39973
 R/Klemenz, M.J.; McKercher, S.R.; Maki, R.A.
 Nucleic Acids Res. 15, 9600, 1987
 A/Title: Nucleotide sequence of the mouse hck gene.
 A/Reference number: A27282; MUID:86067781; PMID:3684607
 A/Accession: A27282
 A/Molecule type: mRNA
 A/Residues: 1-503 <KLE>
 A/Cross-references: GB:Y00487; NID:951209; PIDN:CAA68544.1; PID:951210
 R/Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
 A/Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed
 A/Reference number: A39973; MUID:86068587; PMID:3317404
 A/Accession: A39973
 A/Status: preliminary; not compared with conceptual translation
 A/Residues: 1-503 <HOL>
 A/Molecule type: mRNA
 A/Cross-references: GB:J03023; NID:9192212; PIDN:AAA37305.1; PID:9309118.
 C/Genetics:
 A/Genes: hck
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F/62-110/Domain: SH3 homology <SH3>
 F/121-218/Domain: SH2 homology <SH2>
 F/237-495/Domain: protein kinase homology <KIN>
 F/245-253/Region: protein kinase ATP-binding motif
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/3/Binding site: palmitate (Cys) (covalent) #status predicted
 F/267/Active site: lys #status predicted
 F/388/499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 53.8%; Score 240; DB 1; Length 503;
 Best Local Similarity 56.6%; Pred. No. 1,4e-19;
 Matches 47; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

Qy 1 WLVEGLSRKAEELLPGNPGAFILRESOTRSGSYSLVSLSPADIRHYRHCL 60
 Db 121 WPKGISRKDAERHLAPGNMGLSPFMRDSSTTNGSYSLSVKDFPDGHTVKKIKRRL 180

Qy 61 DNGWLYSPRLTPSLQALVDHY 83
 Db 181 DSGGYISPRITPSPQLALVDHY 203

RESULT 8
 137206
 protein-tyrosine kinase (EC 2.7.1.112) b1k - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 04-Mar-2000
 C/Accession: I37206; S51647
 R/Jilka, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.
 J. Immunol. 154, 1265-1272, 1995
 A/Title: Molecular cloning, characterization, and chromosomal localization of a human ty
 A/Reference number: I37206; MUID:95123078; PMID:7822795
 A/Accession: I37206
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 1-505 <RES>
 A/Molecule type: mRNA
 A/Cross-references: EMBL:Z33998; NID:9601951; PIDN:CAA63965.1; PID:9601952
 C/Genetics:
 A/Genes: GDB:BLK
 A/Cross-references: GDB:454114; OMIM:191305
 A/Map position: 8p23-8p22
 C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C/Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyro
 F/65-113/Domain: SH3 homology <SH3>
 F/124-220/Domain: SH2 homology <SH2>
 F/239-497/Domain: protein kinase homology <KIN>
 F/247-255/Region: protein kinase ATP-binding motif
 F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/269/Active site: lys #status predicted

Query Match 52.1%; Score 232.5; DB 2; Length 505;
 Best Local Similarity 54.2%; Pred. No. 1e-18;
 Matches 45; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

Qy 1 WLVEGLSRKAEELLPGNPGAFILRESOTRSGSYSLVSLSPADIRHYRHCL 60
 Db 124 WPKGISRKDAERHLAPGNMGLSPFMRDSSTTNGSYSLSVKDFPDGHTVKKIKRRL 182

Qy 61 DNGWLYSPRLTPSLQALVDHY 83
 Db 181 DSGGYISPRITPSPQLALVDHY 205

RESULT 9
 OKRUK
 protein-tyrosine kinase (EC 2.7.1.112) lck - human
 N/Alternate names: kinase-related transforming protein (lck)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 28-Jan-2000
 C/Accession: J00152; S07822; S07200; S01879; S07143; A32797; I57636
 R/Bouyer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.
 Gene 84, 105-113, 1989
 A/Title: Structure of the human lck gene: differences in genomic organisation within src
 A/Reference number: J00152; MUID:90108697; PMID:2558056
 A/Accession: J00152
 A/Molecule type: DNA
 A/Residues: 1-509 <ROU>
 A/Cross-references: EMBL:X14053
 R/Perlmutter, R.M.; Martin, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.
 J. Cell. Biochem. 38, 117-126, 1988
 A/Title: Structure and expression of lck transcripts in human lymphoid cells.
 A/Reference number: S07822; MUID:89123626; PMID:3265417
 A/Accession: S07822
 A/Molecule type: mRNA
 A/Residues: 1-86; 'P', 88-509 <PER>
 A/Cross-references: EMBL:X13523; NID:934294; PIDN:CAA11884.1; PID:934295
 R/Koga, Y.; Caccia, N.; Toyonaga, B.; Spolek, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
 Eur. J. Immunol. 16, 1643-1646, 1986
 A/Title: A human T cell-specific cDNA clone (Y116) encodes a protein with extensive hom
 A/Reference number: S07200; MUID:87133831; PMID:3433153
 A/Accession: S07200
 A/Molecule type: mRNA
 A/Residues: 1-205; 'ASATTP', 212-257, 'RCGW', 262, 'TTT', 266, 'T', 268-281, 'AGRLP', 287-503, 'ST
 A/Cross-references: EMBL:X05027; NID:936807; PIDN:CAA28691.1; PID:936808
 R/Veillette, A.; Foss, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.
 Oncogene Res. 1, 357-374, 1987
 A/Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other n
 A/Reference number: S01879; MUID:88217332; PMID:2855736
 A/Accession: S01879
 A/Molecule type: mRNA
 A/Residues: 368-471, 'H', 473-509 <VEI>
 A/Cross-references: EMBL:X06369; NID:934288; PIDN:CAA29667.1; PID:934289
 R/Trevillian, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Lima, T.J.
 Biochim. Biophys. Acta 888, 286-295, 1986
 A/Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA)
 A/Reference number: S07143; MUID:87000726; PMID:3469486
 A/Accession: S07143
 A/Molecule type: mRNA
 A/Residues: 'A', 376-509 <TRE>
 A/Cross-references: EMBL:X04476; NID:935779; PIDN:CAA28165.1; PID:935780
 R/Takahara, T.; Leung, S.; Geronzi, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.
 Mol. Cell. Biol. 9, 2173-2180, 1989
 A/Title: Structure of the two promoters of the human lck gene: differential accumulation
 A/Reference number: A32797; MUID:89313764; PMID:2767474
 A/Accession: A32797
 A/Molecule type: DNA
 A/Residues: 1-35 <TKX>
 A/Cross-references: GB:M26692; NID:9341523; PIDN:AAA59503.1; PID:9349702
 R/Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
 Mol. Cell. Biol. 8, 3058-3064, 1988
 A/Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
 A/Reference number: I57636; MUID:89036891; PMID:2850479

A:Accession: 157636
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-35, 'VR' <RBS>
A:Cross-references: GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g553522
C:Comment: Protein tyrosine kinases play important roles in the control of cell growth & C:Genetics:
A:Gene: GDB:LCK
A:Cross-references: GDB:119360; OMIM:153390
A:Map position: 1p35-1p34.3
A:Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F:2-509/Product: protein-tyrosine kinase lck #status predicted
F:68-116/Domain: SH3 homology <SH3>
F:127-224/Domain: SH2 homology <SH2>
F:243-501/Domain: protein kinase homology <KIN>
F:251-259/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Binding site: palmitate (Cys) (covalent) #status predicted
F:273/Active site: Lys #status predicted
F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
Query Match 51.1%; Score 228; DB 1; Length 509;
Best Local Similarity 54.2%; Pred. No. 3.3e-18;
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
QY 1 WLVGSLREKAEELLPGNPGAFILRESQTRGSYSLSVRLSRPAMDRIRHYRHCL 60
DB 127 WFFKSLSRKDAERQLAPGNTHGSFLIRSESTAGSFSLSRDPDQNGEVVYKHKIRNL 186
QY 61 DNGMLYISPRITFPGSLQALVDHY 83
DB 187 DNGGYISPRITFPGSLQALVDHY 209

RESULT 10
148845
protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse
N:Alternate names: p56, protein-tyrosine kinase tck
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 03-Mar-2000
C:Accession: 148845; A23639; 157629; 177452
R:Voronova, A.F.; Sefton, B.M.
Nucleotide 319, 682-685, 1986
A:Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A:Reference number: 148845; MUID:86146842; PMID:3081813
A:Accession: 148845
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-509 <VOR1>
A:Cross-references: EMBL:X03533; NID:g54813; PIDN:CAA27234.1; PID:g54814
R:March, J.D.; Peet, R.; Krebs, E.G.; Perlmutter, R.M.
Cell 43, 393-404, 1985
A:Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A:Reference number: A23639; MUID:86079521; PMID:2416464
A:Accession: A23639
A:Molecule type: mRNA
A:Residues: 1-282, 'VP', 285-509 <MAR>
A:Cross-references: GB:M2056; NID:g198763
A:Note: the sequence is revised in GenBank entry M2056, release 116.0, (PIDN:AA59674.1
R:Voronova, A.F.; Adler, H.T.; Sefton, B.M.
Mol. Cell. Biol. 7, 4407-4413, 1987
A:Title: Two lck transcripts containing different 5' untranslated regions are present in
A:Reference number: 157629; MUID:86142832; PMID:3501824
A:Accession: 157629
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <VOR>
A:Cross-references: GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:g198767
R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmutter, R.M.

Mol. Cell. Biol. 8, 3058-3064, 1988
A:Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel
A:Reference number: 157636; MUID:89096891; PMID:2850479
A:Accession: 177452
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-35, 'VR' <GAR>
A:Cross-references: GB:M21511; NID:g198766; PIDN:AAA39422.1; PID:g554186
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro
F:68-116/Domain: SH3 homology <SH3>
F:127-224/Domain: SH2 homology <SH2>
F:243-501/Domain: protein kinase homology <KIN>
F:251-259/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:273/Active site: Lys #status predicted
F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
Query Match 50.9%; Score 227; DB 1; Length 509;
Best Local Similarity 54.2%; Pred. No. 4.3e-18;
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
QY 1 WLVGSLREKAEELLPGNPGAFILRESQTRGSYSLSVRLSRPAMDRIRHYRHCL 60
DB 127 WFFKSLSRKDAERQLAPGNTHGSFLIRSESTAGSFSLSRDPDQNGEVVYKHKIRNL 186
QY 61 DNGMLYISPRITFPGSLQALVDHY 83
DB 187 DNGGYISPRITFPGSLQALVDHY 209

RESULT 11
A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
C:Accession: A40092
R:Dymecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.
Science 247, 332-336, 1990
A:Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.
A:Reference number: A40092; MUID:90117477; PMID:2404338
A:Accession: A40092
A:Molecule type: mRNA
A:Residues: 1-499 <DYM>
A:Cross-references: GB:M30903; NID:g202076; PIDN:AAA40453.1; PID:g202077
C:Genetics:
A:Gene: MGI:B1K
A:Cross-references: MGI:88169
A:Map position: 14:28.0
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
F:59-107/Domain: SH3 homology <SH3>
F:118-214/Domain: SH2 homology <SH2>
F:233-491/Domain: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:263/Active site: Lys #status predicted
Query Match 50.3%; Score 224.5; DB 1; Length 499;
Best Local Similarity 51.8%; Pred. No. 8.1e-18;
Matches 43; Conservative 16; Mismatches 23; Indels 1; Gaps 1;
QY 1 WLVGSLREKAEELLPGNPGAFILRESQTRGSYSLSVRLSRPAMDRIRHYRHCL 60
DB 118 WFFKSLSRKDAERQLAPGNTHGSFLIRSESTAGSFSLSRDPDQNGEVVYKHKIRNL 176
QY 61 DNGMLYISPRITFPGSLQALVDHY 83
DB 177 DNGGYISPRITFPGSLQALVDHY 199

RESULT 12
A39939

protein-tyrosine kinase (EC 2.7.1.112) tk1 [similarity] - chicken

N/Alternate names: kinase-related transforming protein (tk1); T-cell surface antigen ass

C/Species: Gallus gallus (chicken)
C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C/Accession: A42126; A39939

R/Chow, L.M.; Ratcliffe, M.J.; Vellente, A.

Mol. Cell. Biol. 12, 1226-1233, 1992

A/Title: tk1 is the avian homolog of the mammalian lck tyrosine protein kinase gene.

A/Reference number: A42126; PMID:92186854; PMID:1545804

A/Accession: A42126

A/Molecule type: mRNA

A/Residues: 1-88 <CHO>

A/Cross-references: GB:M85043

A/Experimental source: thymus, spleen

A/Note: Sequence extracted from NCBI Backbone (NCBI:88831, NCBI:88833)

R/Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987

A/Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related

A/Reference number: A39939; PMID:88097370; PMID:3321053

A/Accession: A39939

A/Molecule type: mRNA

A/Residues: 52-507 <STR>

A/Cross-references: GB:003579; NID:9212712; PIDN:AAA49081.1; PID:9212713

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho

F:66-114/Domain: SH3 homology <SH3>

F:125-222/Domain: SH2 homology <SH2>

F:241-499/Domain: protein kinase homology <KIN>

F:249-257/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 50.0%; Score 223; DB 1; Length 507;

Best Local Similarity 53.0%; Pred. No. 1,2e-17;

Matches 44; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Db 125 WFKULSRKRAEELLLPGNGAFILRESQTRGSLSVLRSPASMDRIRHYRHC 60

Qy 61 DNGMLYISPRITFSPQLALVDHY 83

Db 185 DNGGYISPRVTFSSLHETVEY 207

RESULT 13

151593 protein-tyrosine kinase (EC 2.7.1.112) yes - Xiphophorus helleri

C/Species: Xiphophorus helleri

C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 18-Feb-2000

C/Accession: 151593

R/Hannig, G.; Ottliffe, S.; Schartl, M.

Oncogene 6, 361-369, 1991

A/Title: Conservation of structure and expression of the c-yes and fyn genes in lower ve

A/Reference number: 151592; PMID:91187435; PMID:107152

A/Accession: 151593

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Cross-references: EMBL:X54970; NID:964483; PIDN:CAA38714.1; PID:964484

C/Genetics:

A/Gene: Yyes

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho

F:99-148/Domain: SH3 homology <SH3>

F:159-256/Domain: SH2 homology <SH2>

F:126-534/Domain: protein kinase homology <KIN>

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:306/Active site: lys #status predicted

F:427,538/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 48.7%; Score 217; DB 2; Length 544;

Best Local Similarity 54.2%; Pred. No. 6.5e-17;

Matches 45; Conservative 9; Mismatches 29; Indels 0; Gaps 0;

Qy 1 WLYGSLREKAEELLLPGNGAFILRESQTRGSLSVLRSPASMDRIRHYRHC 60

Db 159 WFKULSRKRAEELLLPGNGAFILRESQTRGSLSVLRSPASMDRIRHYRHC 218

Qy 61 DNGMLYISPRITFSPQLALVDHY 83

Db 219 DNGGYISPRVTFSSLHETVEY 241

RESULT 14

151501 protein-tyrosine kinase (EC 2.7.1.112) Yes [similarity] - African clawed frog

N/Alternate names: kinase-related transforming protein (yes)

C/Species: Xenopus laevis (African clawed frog)

C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C/Accession: A45501; S08517

R/Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.

Oncogene Res. 1, 223-233, 1989

A/Title: The yes proto-oncogene is present in amphibians and contributes to the maternal

A/Reference number: A45501

A/Accession: A45501

A/Molecule type: mRNA

A/Residues: 1-537 <STR>

A/Cross-references: GB:X14377

A/Status: 1-537 <STR>

A/Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro

F:92-141/Domain: SH3 homology <SH3>

F:152-249/Domain: SH2 homology <SH2>

F:269-527/Domain: protein kinase homology <KIN>

F:277-285/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:299/Active site: lys #status predicted

F:420,531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 48.2%; Score 215; DB 1; Length 537;

Best Local Similarity 50.0%; Pred. No. 1.1e-16;

Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

Qy 1 WLYGSLREKAEELLLPGNGAFILRESQTRGSLSVLRSPASMDRIRHYRHC 55

Db 152 WFKULSRKRAEELLLPGNGAFILRESQTRGSLSVLRSPASMDRIRHYRHC 206

Qy 56 RHICDNGMYISPRITFSPQLALVDHY 83

Db 207 KIRKLDNGGYITTRAFESLQKLVHY 234

RESULT 15

151593 protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73

C/Species: avian sarcoma virus Y73

A/Note: host Gallus gallus (chicken)

C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 23-Feb-1997

C/Accession: A00633

R/Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.

Nature 297, 205-208, 1982

A/Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its transf

A/Reference number: A00633; PMID:82195528; PMID:6281656

A/Accession: A00633

A/Molecule type: genomic RNA

A/Residues: 1-528 <KTT>

C/Comment: This protein is synthesized as a gag-yes polypeptide.

C;Genetics:

A: Gene: ♦ yes
C: Superfam:

Cysuperfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
C keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; transferase
E-98-117/Domein_csu_homologues.csu

F;88-137/Domain: SH3 homology <SH3>
E;148-245/Domain: SH2 homology <SH2>

F;148-245/Domain: SH2 homology <SH2>
F;265-523/Domain: protein kinase hom

F;273-281/Region: protein kinase ATP-binding motif

F:295/Active site: Lys #status predicted

F;416/Binding site: phosphate (Tyr) (cov

Query Match 48.0%: Scores

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Query Match      48.0%; Score 214; DB 1; Length 528;
Best Local Similarity 50.0%; Pred. NO. 1 4e-16:

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Best Local Similarity 50.0%; Pred. NO. 1.4e-16;
Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

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QY 1 WLYEGLSREKAEELLLPBNPGAFILIRESQTRGSSLSVRLSRPASWDRIR-----HY 55

148 WYCKMPCBAPIITNOCBOCTEIMCECTHCAVOTCTD
TAMEMOCTHCTHCTD

DB 148 WYFGKMGKDAERLLLPNGNGRGI FLVRESEITTKGAYSLIR-----DWDEVRGDNVKHY 202

QY 56 RHCLDNGWLYISPRLTFFPSLOALVDHY 83

[illegible]

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